

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1653HXP

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 FEB 27 New STN AnaVist pricing effective March 1, 2006
NEWS 4 APR 04 STN AnaVist \$500 visualization usage credit offered
NEWS 5 MAY 10 CA/CAPLUS enhanced with 1900-1906 U.S. patent records
NEWS 6 MAY 11 KOREAPAT updates resume
NEWS 7 MAY 19 Derwent World Patents Index to be reloaded and enhanced
NEWS 8 MAY 30 IPC 8 Rolled-up Core codes added to CA/CAPLUS and
USPATFULL/USPAT2
NEWS 9 MAY 30 The F-Term thesaurus is now available in CA/CAPLUS
NEWS 10 JUN 02 The first reclassification of IPC codes now complete in
INPADOC
NEWS 11 JUN 26 TULSA/TULSA2 reloaded and enhanced with new search and
and display fields
NEWS 12 JUN 28 Price changes in full-text patent databases EPFULL and PCTFULL
NEWS 13 JUL 11 CHEMSAFE reloaded and enhanced
NEWS 14 JUL 14 FSTA enhanced with Japanese patents
NEWS 15 JUL 19 Coverage of Research Disclosure reinstated in DWPI
NEWS 16 AUG 09 INSPEC enhanced with 1898-1968 archive
NEWS 17 AUG 28 ADISCTI Reloaded and Enhanced

NEWS EXPRESS JUNE 30 CURRENT WINDOWS VERSION IS V8.01b, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 26 JUNE 2006.

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS LOGIN Welcome Banner and News Items
NEWS IPC8 For general information regarding STN implementation of IPC 8
NEWS X25 X.25 communication option no longer available

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 18:38:34 ON 29 AUG 2006

=> file medline, biosis, scisearch, wpids, dgene, embase, biotechds, hcaplus
COST IN U.S. DOLLARS SINCE FILE TOTAL
ENTRY SESSION
FULL ESTIMATED COST 0.84 0.84

FILE 'MEDLINE' ENTERED AT 18:40:45 ON 29 AUG 2006

FILE 'BIOSIS' ENTERED AT 18:40:45 ON 29 AUG 2006

Copyright (c) 2006 The Thomson Corporation

FILE 'SCISEARCH' ENTERED AT 18:40:45 ON 29 AUG 2006

Copyright (c) 2006 The Thomson Corporation

FILE 'WPIDS' ENTERED AT 18:40:45 ON 29 AUG 2006

COPYRIGHT (C) 2006 THE THOMSON CORPORATION

FILE 'DGENE' ENTERED AT 18:40:45 ON 29 AUG 2006

COPYRIGHT (C) 2006 THE THOMSON CORPORATION

FILE 'EMBASE' ENTERED AT 18:40:45 ON 29 AUG 2006

Copyright (c) 2006 Elsevier B.V. All rights reserved.

FILE 'BIOTECHDS' ENTERED AT 18:40:45 ON 29 AUG 2006

COPYRIGHT (C) 2006 THE THOMSON CORPORATION

FILE 'HCAPLUS' ENTERED AT 18:40:45 ON 29 AUG 2006

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

=> e allen,s/au

E1	1	ALLEN ZHANG J/AU
E2	1	ALLEN ZOE/AU
E3	0 -->	ALLEN,S/AU
E4	12	ALLENA M/AU
E5	7	ALLENA MARTA/AU
E6	2	ALLENACH D A/AU
E7	3	ALLENACH DAVID/AU
E8	2	ALLENAUSTIN D/AU
E9	1	ALLENB J/AU
E10	2	ALLENBACH/AU
E11	1	ALLENBACH A/AU
E12	1	ALLENBACH ALYCE/AU

=> e hitz, w/au

E1	15	HITZ WILLIAM DEAN/AU
E2	1	HITZ Y/AU
E3	0 -->	HITZ, W/AU
E4	1	HITZAN R G/AU
E5	1	HITZANIDIS K/AU
E6	1	HITZANIDIS KYRIAKOS/AU
E7	2	HITZBLECH T/AU
E8	1	HITZBLECK E/AU
E9	1	HITZBLECK H/AU
E10	7	HITZBLECK J/AU
E11	16	HITZBLECK JULIA/AU
E12	1	HITZBLECK K/AU

=> s beta vulgaris

L1 14669 BETA VULGARIS

=> s l1 and (DNA encoding protein)

5 FILES SEARCHED...

L2 0 L1 AND (DNA ENCODING PROTEIN)

=> s l1 and (sugar transplant protein)

L3 0 L1 AND (SUGAR TRANSPLANT PROTEIN)

=> s (beta vulgaris sugar transport protein)
L4 5 (BETA VULGARIS SUGAR TRANSPORT PROTEIN)

=> d 14 ti abs ibib tot

L4 ANSWER 1 OF 5 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta
vulgaris-like sugar transport protein, for altering the level of
expression of a sugar transport protein in a host cell.
AN 2006-055117 [06] WPIDS
CR 2002-453364 [48]; 2003-340957 [32]
AB US2005282278 A UPAB: 20060124
NOVELTY - An isolated nucleic acid fragment encoding all or a substantial
portion of an Arabidopsis thaliana-like sugar transport protein, is new.
DETAILED DESCRIPTION - A new isolated nucleic acid fragment encodes
all or a substantial portion of an Arabidopsis thaliana-like sugar
transport protein comprising a member selected from:
(A) an isolated nucleic acid fragment encoding all or a substantial
portion of the amino acid sequence set forth in a member selected from SEQ
ID NO: 2, 4, 6, 8, 10, 12, 14 and 16, given in the specification;
(B) an isolated nucleic acid fragment that is substantially similar
to an isolated nucleic acid fragment encoding all or a substantial portion
of the amino acid sequence set forth in a member selected from SEQ ID NO:
2, 4, 6, 8, 10, 12, 14 and 16; and
(C) an isolated nucleic acid fragment that is complementary to (a) or
(b).
INDEPENDENT CLAIMS are also included for:
(1) an isolated nucleic acid fragment encoding all or a substantial
portion of an Beta vulgaris-like sugar transport protein comprising a
member selected from:
(i) an isolated nucleic acid fragment encoding all or a substantial
portion of the amino acid sequence set forth in a member selected from the
group consisting of SEQ ID NO:18, 20, 22, 24, 26 and 28, given in the
specification;
(ii) an isolated nucleic acid fragment that is substantially similar
to an isolated nucleic acid fragment encoding all or a substantial portion
of the amino acid sequence set forth in a member selected from SEQ ID
NO:18, 20, 22, 24, 26 and 28; and
(iii) an isolated nucleic acid fragment that is complementary to or
(b);
(2) a chimeric gene comprising the nucleic acid fragment operably
linked to suitable regulatory sequences;
(3) a transformed host cell comprising the chimeric gene;
(4) an Arabidopsis thaliana-like sugar transport protein polypeptide
comprising all or a substantial portion of the amino acid sequence cited;
(5) a Beta vulgaris sugar
transport protein polypeptide comprising all or a
substantial portion of the amino acid sequence cited;
(6) a method of altering the level of expression of a sugar transport
protein in a host cell;
(7) a method of obtaining a nucleic acid fragment encoding all or a
substantial portion of the amino acid sequence encoding a sugar transport
protein; and
(8) the product of the obtaining method.

USE - The nucleic acid fragment is useful for altering the level of
expression of a sugar transport protein in a host cell (claimed).

Dwg.0/2

ACCESSION NUMBER: 2006-055117 [06] WPIDS
CROSS REFERENCE: 2002-453364 [48]; 2003-340957 [32]
DOC. NO. CPI: C2006-020697
TITLE: New nucleic acid fragment encoding a Arabidopsis
thaliana-like or Beta vulgaris-like sugar transport

protein, for altering the level of expression of a sugar transport protein in a host cell.

DERWENT CLASS: C06 D16
INVENTOR(S): ALLEN, S M; HITZ, W D; KINNEY, A J; TINGEY, S V
PATENT ASSIGNEE(S): (ALLE-I) ALLEN S M; (HITZ-I) HITZ W D; (KINN-I) KINNEY A J; (TING-I) TINGEY S V
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2005282278	A1	20051222	(200606)*		59

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2005282278	A1 Div ex	US 2002-51902	20020117
		US 2005-210316	20050824

PRIORITY APPLN. INFO: US 2002-51902 20020117; US
2005-210316 20050824

L4 ANSWER 2 OF 5 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.

AN 2003-340957 [32] WPIDS
CR 2002-453364 [48]; 2006-055117 [06]
AB US2002178468 A UPAB: 20060124

NOVELTY - An Arabidopsis thaliana-like sugar transport protein (I) and a Beta vulgaris sugar transport protein (II), where (I) comprises eight fully defined sequences of, e.g. 747, 131, 131, and 737 amino acids in length and (II) comprises six fully defined sequences of, e.g. 167, 513, 510 and 523 amino acids in length, are new. Sequences given in the specification.

DETAILED DESCRIPTION - (I) comprises all or a substantial portion of the fully defined sequences of 747, 131, 131, 737, 486, 117, 345 and 228 amino acids in length and (II) comprises all or a substantial portion of the fully defined sequences of 167, 513, 510, 523, 539 and 529 amino acids in length.

INDEPENDENT CLAIMS are also included for:

- (1) An isolated nucleic acid fragment (III)-(IV) comprising:
 - (a) A fragment encoding (I) or (II), respectively;
 - (b) A nucleic acid fragment that is similar to (III)-(IV), and
 - (c) An isolated nucleic acid fragment that is complementary to (III)-(IV);
- (2) A chimeric gene (V) comprising (III) or (IV) operably linked to suitable regulatory sequences;
- (3) A transformed host cell (VI) comprising (V);
- (4) Obtaining (M1) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising:
 - (a) synthesizing an oligonucleotide primer corresponding to a portion of the nucleic acid sequence of (III) or (IV);
 - (b) amplifying a cDNA insert present in a cloning vector using the primers and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein;
- (5) Obtaining (M2) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising:

(a) probing a cDNA or genomic library with (III) or (IV);
(b) identifying a DNA clone that hybridizes with (III) or (IV);
(c) isolating the DNA clone; and
(d) sequencing the cDNA or genomic fragment that comprise the clone;
and

(6) The product of (M1) and (M2).

USE - The polypeptides may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with the chimeric construct (claimed). Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants.

Dwg.0/2

ACCESSION NUMBER: 2003-340957 [32] WPIDS
CROSS REFERENCE: 2002-453364 [48]; 2006-055117 [06]
DOC. NO. NON-CPI: N2003-272743
DOC. NO. CPI: C2003-089353
TITLE: Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): ALLEN, S M; HITZ, W D; KINNEY, A J; TINGEY, S V
PATENT ASSIGNEE(S): (ALLE-I) ALLEN S M; (HITZ-I) HITZ W D; (KINN-I) KINNEY A J; (TING-I) TINGEY S V
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002178468	A1	20021128	(200332)*		56

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2002178468	A1 Provisional	US 1998-83044P	19980424
	Div ex	US 1999-291922	19990414
		US 2002-51902	20020117

FILING DETAILS:

PATENT NO	KIND	PATENT NO
US 2002178468	A1 Div ex	US 6383776

PRIORITY APPLN. INFO: US 1998-83044P 19980424; US
1999-291922 19990414; US
2002-51902 20020117

L4 ANSWER 3 OF 5 DGENE COPYRIGHT 2006 The Thomson Corp on STN
TI New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell.
AN AEE68545 protein DGENE
AB The invention comprise the amino acid and coding sequences of sugar transport proteins. The DNA and protein sequences of the invention are useful for altering the level of expression of a sugar transport protein in a host cell. The present amino acid sequence represents a sugar transport protein that was used in an example of the invention.

ACCESSION NUMBER: AEE68545 protein DGENE
TITLE: New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell.

INVENTOR: Allen S M; Hitz W D; Kinney A J; Tingey S V
PATENT ASSIGNEE: (ALLE-I) ALLEN S M.
(HITZ-I) HITZ W D.
(KINN-I) KINNEY A J.
(TING-I) TINGEY S V.
PATENT INFO: US 2005282278 A1 20051222 59
APPLICATION INFO: US 2005-210316 20050824
PRIORITY INFO: US 2002-51902 20020117
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2006-055117 [06]
DESCRIPTION: Beta vulgaris sugar
transport protein amino acid sequence - SEQ
ID 30.

L4 ANSWER 4 OF 5 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta
vulgaris-like sugar transport protein, for altering the level of
expression of a sugar transport protein in a host cell;
plant recombinant protein isolation via transformed host cell for use
in protein expression alteration
AN 2006-03652 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - An isolated nucleic acid fragment encoding all or a substantial
portion of an Arabidopsis thaliana-like sugar transport protein, is new.
DETAILED DESCRIPTION - A new isolated nucleic acid fragment encodes
all or a substantial portion of an Arabidopsis thaliana-like sugar
transport protein comprising a member selected from: (A) an isolated
nucleic acid fragment encoding all or a substantial portion of the amino
acid sequence set forth in a member selected from SEQ ID NO: 2, 4, 6, 8,
10, 12, 14 and 16, given in the specification; (B) an isolated nucleic
acid fragment that is substantially similar to an isolated nucleic acid
fragment encoding all or a substantial portion of the amino acid sequence
set forth in a member selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 and
16; and (C) an isolated nucleic acid fragment that is complementary to
(a) or (b). INDEPENDENT CLAIMS are also included for: (1) an isolated
nucleic acid fragment encoding all or a substantial portion of an Beta
vulgaris-like sugar transport protein comprising a member selected from:
(i) an isolated nucleic acid fragment encoding all or a substantial
portion of the amino acid sequence set forth in a member selected from
the group consisting of SEQ ID NO: 18, 20, 22, 24, 26 and 28, given in the
specification; (ii) an isolated nucleic acid fragment that is
substantially similar to an isolated nucleic acid fragment encoding all
or a substantial portion of the amino acid sequence set forth in a member
selected from SEQ ID NO: 18, 20, 22, 24, 26 and 28; and (iii) an isolated
nucleic acid fragment that is complementary to or (b); (2) a chimeric
gene comprising the nucleic acid fragment operably linked to suitable
regulatory sequences; (3) a transformed host cell comprising the chimeric
gene; (4) an Arabidopsis thaliana-like sugar transport protein
polypeptide comprising all or a substantial portion of the amino acid
sequence cited; (5) a Beta vulgaris sugar
transport protein polypeptide comprising all or a
substantial portion of the amino acid sequence cited; (6) a method of
altering the level of expression of a sugar transport protein in a host
cell; (7) a method of obtaining a nucleic acid fragment encoding all or a
substantial portion of the amino acid sequence encoding a sugar transport
protein; and (8) the product of the obtaining method.
BIOTECHNOLOGY - Preferred Method: Altering the level of expression
of a sugar transport protein in a host cell comprises transforming a host
cell with the chimeric gene, and growing the transformed host cell
produced under conditions that are suitable for expression of the
chimeric gene, where expression of the chimeric gene results in
production of altered levels of a sugar transport protein in the

transformed host cell. Obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a sugar transport protein comprises: (a) probing a cDNA or genomic library with the nucleic acid fragment; (b) identifying a DNA clone that hybridizes with the nucleic acid fragment; (c) isolating the DNA clone identified; and (d) sequencing the cDNA or genomic fragment that comprises the clone isolated, where the sequenced nucleic acid fragment encodes all or a substantial portion of the amino acid sequence encoding a sugar transport protein. The method alternatively comprises synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in any of SEQ ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein.

USE - The nucleic acid fragment is useful for altering the level of expression of a sugar transport protein in a host cell (claimed). (59 pages)

ACCESSION NUMBER: 2006-03652 BIOTECHDS

TITLE: New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell;
plant recombinant protein isolation via transformed host cell for use in protein expression alteration

AUTHOR: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V

PATENT ASSIGNEE: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V

PATENT INFO: US 2005282278 22 Dec 2005

APPLICATION INFO: US 2005-210316 24 Aug 2005

PRIORITY INFO: US 2005-210316 24 Aug 2005; US 2002-51902 17 Jan 2002

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2006-055117 [06]

L4 ANSWER 5 OF 5 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN

TI Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein;
involving vector plasmid-mediated gene transfer and expression in host cell for use in carbohydrate transport control

AN 2003-14205 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - An Arabidopsis thaliana-like sugar transport protein (I) and a Beta vulgaris sugar transport protein (II), where (I) comprises eight fully defined sequences of, e.g. 747, 131, 131, and 737 amino acids in length and (II) comprises six fully defined sequences of, e.g. 167, 513, 510 and 523 amino acids in length, are new. Sequences given in the specification.

DETAILED DESCRIPTION - (I) comprises all or a substantial portion of the fully defined sequences of 747, 131, 131, 737, 486, 117, 345 and 228 amino acids in length and (II) comprises all or a substantial portion of the fully defined sequences of 167, 513, 510, 523, 539 and 529 amino acids in length. INDEPENDENT CLAIMS are also included for: (1) An isolated nucleic acid fragment (III)-(IV) comprising: (a) A fragment encoding (I) or (II), respectively; (b) A nucleic acid fragment that is similar to (III)-(IV), and (c) An isolated nucleic acid fragment that is complementary to (III)-(IV); (2) A chimeric gene (V) comprising (III) or (IV) operably linked to suitable regulatory sequences; (3) A transformed host cell (VI) comprising (V); (4) Obtaining (M1) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising: (a) synthesizing an oligonucleotide primer corresponding to a portion of the nucleic acid sequence of (III)

or (IV); (b) amplifying a cDNA insert present in a cloning vector using the primers and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein; (5) Obtaining (M2) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising: (a) probing a cDNA or genomic library with (III) or (IV); (b) identifying a DNA clone that hybridizes with (III) or (IV); (c) isolating the DNA clone; and (d) sequencing the cDNA or genomic fragment that comprise the clone; and (6) The product of (M1) and (M2).

BIOTECHNOLOGY - Preparation: The proteins may be prepared according to standard recombinant methodologies.

USE - The polypeptides may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with the chimeric construct (claimed). Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants.

EXAMPLE - cDNA libraries representing mRNAs from various corn, rice, soybean and wheat tissues were prepared. The cDNAs were introduced into plasmid vectors by first preparing the cDNA libraries in Uni-ZAP XR vectors. The Uni-ZAP XR libraries were converted into plasmid libraries. The cDNAs were introduced directly into precut Bluescript vectors. Once the cDNA inserts were in plasmid vectors, the insert cDNA sequences were amplified by polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Insert DNAs were sequenced in dye-primer sequencing reactions to generate partial cDNA sequences. The resulting expressed sequence tags (ESTs) were analyzed using a sequencer. ESTs encoding sugar transport proteins were identified by conducting BLAST. The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the nr database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the nr database using the BLASTX algorithm provided by the NCBI. The BLASTX search using EST sequences from several corn, rice, soybean and wheat clones revealed similarity of the proteins encoded by the cDNAs to a sugar transport protein from *Arabidopsis thaliana*. In the process of comparing the ESTs it was found that many of the clones had overlapping regions of homology. Using this homology it was possible to align the ESTs and assemble and wheat sugar transport proteins. The sequence of the corn contig composed of clones p0032.crcba66r, p0097, cgran41r, crln.pk0143.h10, p0128, cpict38, p0106, cj1pm67r, cillc.pk001.f21, p0072comgi92r, p0114, cimml81r and p0002.cgevb73r was 2824 nucleotides. The sequence of rice contig composed of clones r1r12.pk0013.d11 and rds1c.pk007.n17 was 443 nucleotides. The sequence of the entire cDNA inserts from clone r1s6.pk0003.d5 was 870 nucleotides fully defined in the specification. Similarly, *Beta vulgaris* sugar transport proteins were also identified and characterized. (56 pages)

ACCESSION NUMBER: 2003-14205 BIOTECHDS

TITLE: Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein; involving vector plasmid-mediated gene transfer and expression in host cell for use in carbohydrate transport control

AUTHOR: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V

PATENT ASSIGNEE: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V

PATENT INFO: US 2002178468 28 Nov 2002

APPLICATION INFO: US 2002-51902 17 Jan 2002

PRIORITY INFO: US 2002-51902 17 Jan 2002; US 1998-83044 24 Apr 1998

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2003-340957 [32]

=> d his

(FILE 'HOME' ENTERED AT 18:38:34 ON 29 AUG 2006)

FILE 'MEDLINE, BIOSIS, SCISEARCH, WPIDS, DGENE, EMBASE, BIOTECHDS, HCAPLUS' ENTERED AT 18:40:45 ON 29 AUG 2006

E ALLEN, S/AU

E HITZ, W/AU

L1 14669 S BETA VULGARIS

L2 0 S L1 AND (DNA ENCODING PROTEIN)

L3 0 S L1 AND (SUGAR TRANSPLANT PROTEIN)

L4 5 S (BETA VULGARIS SUGAR TRANSPORT PROTEIN)

=> s l1 and (DNA fragment)

L5 27 L1 AND (DNA FRAGMENT)

=> s l5 and (sugar transport protein)

L6 0 L5 AND (SUGAR TRANSPORT PROTEIN)

=> s l5 and (regulatory sequence)

UNMATCHED LEFT PARENTHESIS 'AND (REGULATORY'

The number of right parentheses in a query must be equal to the number of left parentheses.

=> s l5 and (regulatory sequence)

5 FILES SEARCHED...

L7 0 L5 AND (REGULATORY SEQUENCE)

=> s l5 and (protein)

L8 10 L5 AND (PROTEIN)

=> d l8 ti abs ibib tot

L8 ANSWER 1 OF 10 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN

TI RECOMBINANT BEET CURLY TOP VIRUS GENOMES EXHIBIT BOTH PARENTAL AND NOVEL PATHOGENIC PHENOTYPES

AB Recombinant genomes derived from the Logan and CFH strains of the geminivirus beet curly top virus (BCTV) have been constructed and analyzed for pathogenicity on *Nicotiana benthamiana* and sugar beet (*Beta vulgaris* L.). Infectivity assays indicated that the latent period on *N. benthamiana* was primarily determined by a DNA fragment bearing the leftward open reading frames (ORFs) L1, L2, L3, and L4. Recombinants bearing leftward ORFs from the CFH strain were characterized as having a short latent period (mean = 6-11 days), while the reciprocal recombinants bearing leftward ORFs from the Logan strain had latent periods defined as long (mean = 16-22 days). Infectivity assays on sugar beet indicated that certain recombinant BCTV genomes exhibited novel pathogenic properties not common to either wild type strain, including the loss of systemic movement and replication competency, or asymptomatic systemic infection of sugar beet. The results indicate that *N. benthamiana* is a more permissive host than sugar beet with respect to heterologous combinations of BCTV genes, and that pathogenicity and virulence of BCTV in sugar beet requires the interaction of certain viral gene products and/or cis-elements that have coevolved in the same strain. (C) 1994 Academic Press, Inc.

ACCESSION NUMBER: 1994:244572 SCISEARCH

THE GENUINE ARTICLE: NG523

TITLE: RECOMBINANT BEET CURLY TOP VIRUS GENOMES EXHIBIT BOTH PARENTAL AND NOVEL PATHOGENIC PHENOTYPES

AUTHOR: STENGER D C (Reprint); DAVIS K R; BISARO D M
 CORPORATE SOURCE: NO ILLINOIS UNIV, DEPT BIOL SCI, DE KALB, IL 60115
 (Reprint); OHIO STATE UNIV, CTR BIOTECHNOL, COLUMBUS, OH
 43210; OHIO STATE UNIV, DEPT PLANT BIOL, COLUMBUS, OH
 43210; OHIO STATE UNIV, DEPT MOLEC GENET, COLUMBUS, OH
 43210
 COUNTRY OF AUTHOR: USA
 SOURCE: VIROLOGY, (1 MAY 1994) Vol. 200, No. 2, pp. 677-685.
 ISSN: 0042-6822.
 PUBLISHER: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE
 1900, SAN DIEGO, CA 92101-4495.
 DOCUMENT TYPE: Article; Journal
 FILE SEGMENT: LIFE
 LANGUAGE: English
 REFERENCE COUNT: 47
 ENTRY DATE: Entered STN: 1994
 Last Updated on STN: 1994
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L8 ANSWER 2 OF 10 DGENE COPYRIGHT 2006 The Thomson Corp on STN
 TI Novel DNA used to produce transgenic plants with altered floral
 regulation which can have increased crop yields -
 AN AAZ36962 DNA DGENE
 AB The present sequence encodes a partial protein having a
 flowering regulating activity. Such proteins from Arabidopsis and rice
 are also disclosed, and are designated designated MPC1 and Os-MPC1,
 respectively. The rice and Arabidopsis cDNAs show significant homology
 with each other. A naturally occurring mutation of the MPC1 gene
 eliminates normal flowering regulating ability of plants, and leads to
 flowering immediately after germination (super early flowering mutation).
 The MPC1 polynucleotide sequence can be used to produce plants with
 altered flowering times in comparison with wild type plants, by enhancing
 or inhibiting the expression of the flowering regulating gene. Antisense
 polynucleotides can be used to reproduce the effects of the mutated MPC1
 gene. This alteration can be used to increase the yield of food crops.
 Flowering inhibition of vegetables increases their productivity.

ACCESSION NUMBER: AAZ36962 DNA DGENE
 TITLE: Novel DNA used to produce transgenic plants with altered
 floral regulation which can have increased crop yields -
 INVENTOR: Yoshida N; Kato Y; Takahashi S; Yanai Y; Hiratsuka J; Miwa T
 PATENT ASSIGNEE: (MITA)MITSUI CHEM INC.
 PATENT INFO: EP 967278 A2 19991229 53
 APPLICATION INFO: EP 1999-305077 19990628
 PRIORITY INFO: JP 1998-180065 19980626
 JP 1999-179043 19990624
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 OTHER SOURCE: 2000-064612 [06]
 CROSS REFERENCES: P-PSDB: AAY53934
 DESCRIPTION: DNA fragment encoding a flowering
 regulating protein.

L8 ANSWER 3 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
 TI Utilizing DNA containing all nucleotide sequences of spacer region of
 rDNA and whose G and C content exceeds 50% as enhancer which activates
 promoter of foreign cell;
 new enhancer for use in transgenic plant construction
 AN 2003-27031 BIOTECHDS
 AB DERWENT ABSTRACT:
 NOVELTY - Utilizing (M1) DNA (I) containing all the nucleotides sequences
 of spacer region of ribosomal DNA (rDNA), nucleotide sequence containing
 repeated rDNA spacer region sequence, or nucleotide sequence originating
 from the sequence and the total amount of G+C content exceeds 50%, as

enhancer which activates the promoter of a foreign cell.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) increasing (M2) expression in one or more foreign cell in one or more organ of plant by increasing activity of the promoter of one or more foreign gene involves use of (I); (2) chimeric gene (II) containing (I) and gene promoter, coding sequence or non-coding sequence and terminator sequence; (3) transformed plant (III) containing (II); and (4) cell in which expression of foreign gene is increased by (M1) and (M2).

BIOTECHNOLOGY - Preferred Method: In (M1), (I) hybridizes at 65degreesC in hybridization solution which consists of 3XSSC, 20 mM NaPO₄ (pH 6.8) and is washed at 65degreesC in washing solution of 0.2X SSC, (I) hybridizes to DNA containing entire nucleotide sequences of spacer region of rDNA and nucleotide sequence comprising repeated rDNA spacer region, whose total amount of G+C content exceed 50%. Each of G and C is at least 25%, 30%, or 35%. (I) is derived from rice. (I) is isolated and/or purified DNA. In (M2), (I) is obtained from plant gene or produced artificially. Gene promoter is a promoter of plant. (I) increases the expression of green or non-green tissue of plant gene specifically in root, tuber, seed, stalk, flower or leaf of plant. The enhancer acts in both normal direction and reverse direction. A terminator is coupled with gene promoter. (III) is chosen from potato, tobacco, cotton, lettuce, melon, pumpkin, cucumber, pea, Brassica campestris (rapeseed plant), soybeans, sugar beet Helianthus annuus (sunflower), wheat, barley, rye wheat, rice, or maize.

USE - (I) is useful as an enhancer which activates the promoter of foreign cell. (M2) is useful for increasing gene expression in one or more foreign cell in one or more organ of a plant by increasing activity of a promoter of one or more foreign gene (claimed).

ADVANTAGE - The spacer region of rDNA with a high G+C content as enhancer increases the expression of foreign gene.

EXAMPLE - Expression of chimeric gene in transformed rice plant, which encode NADP type malic-acid enzyme was as follows. Amel cDNA which encoded NADP type malic-acid enzyme of aloe was isolated from pBluescript SK+ by digesting the vector with SmaI and KpnI. pLHC4 plasmid was digested by HindIII and SmaI, Cab promoter region was isolated. The DNA fragment of Cab promoter and cDNA of Amel were simultaneously cloned into pUC19. The obtained plasmid pUC19 was further cut by HindIII and SacI. The DNA fragment containing Cab promoter region and Amel cDNA were cloned to pBI-HI vector in which beta glucuronidase (GUS) gene was removed, where the hygromycin resistant gene is contained in pBI-HI. The obtained expression vector was named pBI-MC. The spacer region (3.2 kb) containing 25S rDNA(s) and a part of 17S rDNA(s) was obtained from pRR217 plasmid by digesting the plasmid with EcoRI and BamHI. The spacer region was cloned into pBluescript SK+. The obtained pBluescript SK+ was digested by XhoI and XbaI and 3.2 kb fragment obtained, was cloned into pUC19, and named pUC-SP. pUC-SP was digested by Sse8387I and XbaI and 3.2 kb fragment was obtained. The fragment was inserted into upstream of Cab promoter of pBI-MC. The expression vector was named pBI-MC/SP3.2. Agrobacterium tumefaciens was transformed with expression vector pBI-MC/SP3.2 and then was made to infect rice callus. Transformed rice callus was selected, after eliminating Agrobacterium, using hygromycin. A plant was regenerated from the selected resistant callus. In liquid nitrogen, leaves of transformed plant was fragmented, ground in 1.5 ml extraction buffer and centrifuged for 5 minutes at 15000 rpm at 4degreesC. The supernatant liquid was used as crude-enzyme liquid. To 50 mul of crude-enzyme liquid, 5 ml of sodium maleate aqueous solution was added and enzyme activity was computed from change of absorbance at 340 nm. The enzyme activity of six rice plants which had expression vector pBI-MC which did not contain the spacer area of rice rDNA and enzyme activity of eight rice plant which had expression vector pBI-MC/SP3.2 which contained the spacer region were compared. The results conformed that the spacer region was functioning as an enhancer

which increased expression of exogenous chimeric gene. (10 pages)
ACCESSION NUMBER: 2003-27031 BIOTECHDS
TITLE: Utilizing DNA containing all nucleotide sequences of spacer
region of rDNA and whose G and C content exceeds 50% as
enhancer which activates promoter of foreign cell;
new enhancer for use in transgenic plant construction
PATENT ASSIGNEE: MITSUI CHEM INC
PATENT INFO: JP 2003135067 13 May 2003
APPLICATION INFO: JP 2001-332861 30 Oct 2001
PRIORITY INFO: JP 2001-332861 30 Oct 2001; JP 2001-332861 30 Oct 2001
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
OTHER SOURCE: WPI: 2003-771330 [73]

L8 ANSWER 4 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Novel herbicide resistant transformed sugar beet detectable by the
specific primers to match the DNA sequences that flank the left and/or
right border region of the inserted DNA;
plasmid pMON17227-mediated Agrobacterium sp. phosphoshikimate-1-
carboxyvinyltransferase gene transfer for herbicide resistance
sugarbeet transgenic plant construction
AN 2002-19740 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - The transgenic glyphosate resistant sugar beet (I) comprising
an insertion of DNA unique to T227-1 and its progeny detectable by either
of the pair of primers for the left or right border, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
following: (1) a pair of primers (II) comprising DNA which flank one of
the border regions of the insertion of DNA into the T227-1 event; and (2)
a polymerase chain reaction test using (II).
BIOTECHNOLOGY - Preferred Sugar Beet: (I) is detectable with the
pair of primers identified as 98G94 and 98K86, 98150 and 98K89 or
98K89-RB12. (I) is detectable with the pair of primers that produce a
fragment selected from 246 base pairs, 476 base pairs or 792 base pairs.
(I) is characterized by an unique sequence of DNA having at least 80%
homology to the right or left border sequence comprising genomic sugar
beet DNA proximate the breakpoint of the insertion of the DNA into the
genome and inserted plasmid DNA, where at least a 20 base pair fragment
of the sequence of DNA is capable of detection by a pair of flanking
primers where one of the primers is developed from the genomic sugar beet
DNA proximate the breakpoint of the insertion of the DNA into the genome
and one of the primers being developed from the inserted DNA plasmid.
Preferred Primer: (II) comprises a DNA which lies in right border region
of the insertion of DNA into the T227-1 event, where one primer lies in
the plant genomic material and the other primer is in the inserted
plasmid material. (II) comprises a DNA which lies in left border region
of the insertion of DNA into the T227-1 event.
USE - (II) is useful in PCR (polymerase chain reaction)
amplification to detect the presence or absence of the T227-1 event. (II)
is also useful for detecting T227-1 event, by selecting sugar beet
genomic material, employing the pair of primers capable of detecting the
T227-1 event in association with such selected material, using a PCR
machine to amplify the DNA fragment if it exists, and
detecting the presence or the absence of the DNA
fragment. (II) is also useful for detecting (I) characterized by
T227-1 event with a test, by selecting sugar beet genomic material for
testing, forming a pair of primers flanking the border sequence, where
the primers are capable of detecting the glyphosate resistant sugar,
using a PCR machine to amplify a unique DNA fragment
produced through the use of the primers, if such fragment can be
produced, and detecting the presence or absence of the DNA
fragment (claimed).
EXAMPLE - The plasmid contained the left border, right border, the

FMV 35S promoter (from a modified figwort mosaic virus), and the main gene of interest to give glyphosate resistance the CP4 syn: the 5-enolpyruvylshikimate-3-phosphate synthase (CP4 EPSPS) gene from *Agrobacterium* sp. strain CP4. The plasmid also contained a chloroplast transit peptide and a terminator from pea. The circular vector pMON17227 opens at both left and right borders when inserted into the plant genome to form the transformed event. The selected transformation event was the T227-1 event. This transformed beet T227-1 and its progeny show excellent levels of glyphosphate tolerance. To characterize T227-1 fully, providing information that serves as a basis for event-specific polymerase chain reaction tests, the nucleotide sequences of the breakpoints between inserted vector and plant genomic DNA were determined. Genomic sequences flanking the T227-1 insert were isolated by linker PCR. Genomic DNA was digested and linkers attached to the ends of the fragments obtained. The fragments containing the T227-1 sequences were preferentially amplified using the linker sequence and pMON17227-specific sequences primers. The PCR products were sequenced, and the sequences used to design further primers, these were then used to amplify plant genomic DNA from the T227-1 transformant for both left and right borders (flanking sequences PCR) and from an untransformed plant. The first pair of primers was in the right border region of the inserted material. 98k89 was a primer that was located within the sugar beet plant genome. 98150 was a primer that was located in the inserted plasmid DNA sequence. In combination these primers, can be employed to produce a unique piece of DNA through a PCR test. This unique DNA specifically identifies this T227-1 transformation event. The sugar beet identified by this PCR flanking sequence was only the T227-1 event or its progeny. The second pair of primers was in the left border region of the inserted material. 98k86 was a primer that was located within the sugar beet plant genome. 98G94 was a primer that was located in the inserted plasmid DNA sequence. In combination these primers can be employed to produce a unique piece of DNA through a PCR test. These event specific tests using the primers include a method that employs electrophoresis through gels as the standard method used to separate, identify and purify DNA fragments. The location of the DNA that was separated by size within the gels can be determined by using a dye. This dye permits DNA bands with 1-10 ng of DNA to be detected under ultraviolet light. This unique DNA specifically identifies this T227-1 transformation event. The sugar beet identified by this PCR flanking sequence was only the T227-1 event or its progeny. Primers 98K89 and 98K86 for the T227-1 event or its progeny were situated in the regions flanking the inserted sequences, while 98150 and 98G94 lie inside the DNA from the vector. PCR with these primers was performed. In each 50 microl reaction, 50 ng of plant DNA was incubated with 120 ng of each primer and 1 U of Amplitaq DNA polymerase in GeneAmp PCR buffer II containing 10 mM Tris-HCl pH8.3 and 50 mM KCl complemented with 1.5 mM MgCl₂ and 0.2 mM dNTP. 1 PCR reaction consisted of a hot start of 3 min. at 94degreesC followed by 35 cycles (one cycle: 30 seconds. at 94degreesC, 1 min, at 57degreesC and 1 min. at 72degreesC). The PCR products were separated on a 1.5% agarose gel. This amplification clearly demonstrated that the left and right flanking sequences were normally contiguous in sugar beet, and have not suffered major reorganization as a result of the transformation.

(26 pages)

ACCESSION NUMBER: 2002-19740 BIOTECHDS

TITLE: Novel herbicide resistant transformed sugar beet detectable by the specific primers to match the DNA sequences that flank the left and/or right border region of the inserted DNA; plasmid pMON17227-mediated *Agrobacterium* sp. phosphoshikimate-1-carboxyvinyltransferase gene transfer for herbicide resistance sugarbeet transgenic plant construction

AUTHOR: WEYENS G; BARNES S; ROSQUE I

PATENT ASSIGNEE: SES EURO NV

PATENT INFO: WO 2002044407 6 Jun 2002

APPLICATION INFO: WO 2000-GB5321 30 Nov 2000
PRIORITY INFO: US 2000-250110 30 Nov 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-557546 [59]

L8 ANSWER 5 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Novel isolated nucleic acid encoding a promoter which is capable of
driving chemically inducible but not wound- or pathogen-inducible
expression of an associated nucleotide sequence;
recombinant vector plasmid pBSK-mediated lipoxxygenase gene transfer
and expression in host cell and polymerase chain reaction for use as a
fungicide, herbicide and pesticide

AN 2002-10155 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - An isolated nucleic acid molecule (a promoter of rice
chemically induced cDNA (RCI-1) (I) capable of driving
chemically-inducible but not wound- or pathogen-inducible expression of
an associated nucleotide sequence, is new

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the
following: (1) an isolated nucleic acid molecule (II) which hybridizes
under stringent conditions to a fully defined sequence of 358 (S1), 2104
(S2), 1516 (S3), 4569 (S17), 1198 (S18) or 2096 (S19) nucleotides as
given in the specification, or to 4.5 kb PstI fragment (F) of plasmid
pBSK+LOX4A which has been deposited under accession number DSM 13524,
where the nucleic acid molecule drives chemically inducible but not
wound- or pathogen-inducible expression of an operably-linked nucleotide
sequence (2) an isolated nucleic acid molecule (III) which has a
constitutive stretch of at least 50 nucleotides which has at least 70%
sequence identity with a consecutive stretch of at least 50 nucleotides
of (S1)-(S3), (S17)-(S19) or (F) as described above; (3) a recombinant
nucleic acid molecule (IV) comprising (I), (II) or (III), operably linked
to a nucleotide sequence of interest; (4) a nucleic acid expression
vector (V) comprising (I)-(III) or (IV); (5) a host cell (VI) stably
transformed with (I)-(III) or (IV); (6) a plant and its progeny (VII)
stably transformed with (I)-(III) or (IV); (7) producing (I) by a
polymerase chain reaction involves use of at least one oligonucleotide
comprising a sequence of nucleotides which represents a consecutive
stretch of 15 or more nucleotides of (S1)-(S3), (S17), or (S18) or (S19);
(8) an isolated nucleic acid molecule (VIII) encoding a fully defined
sequence of 37 amino acids (S6) as given in the specification, where the
amino acid sequence (a transit peptide) is capable of targeting an
associated protein to plastids; (9) a peptide (IX) encoded by
(VIII); (10) an isolated nucleic acid molecule (X) which hybridizes under
stringent conditions to a fully defined sequence of 3018 nucleotides (S5)
as given in the specification and encodes a protein with
lipoxxygenase activity, where the protein encoded by the DNA has
at least 65% amino acid sequence identity with the amino acid sequence of
922 amino acids (S7) fully defined in the specification; (11) a
protein (XI) encoded by (X); (12) a recombinant nucleic acid
molecule (XII) comprising (VIII) or (X); (13) a host cell stably
transformed with (XII); (14) a plant or its progeny stably transformed
with (XII); and (15) a seed of the above plant or its progeny.

BIOTECHNOLOGY - Preferred Nucleic Acid: . (I) is a component of the
PstI/PstI fragment of about 4.5 kb in length from plasmid pBSK+LOX4A
which has been deposited under Acc.Number DMS 13524. (I) is a component of
the nucleotide sequence which has the fully defined sequence of (S17).
(I) comprises (i) the nucleotide sequence of (S1), (ii) nucleotides
1-1358 of (S2), (iii) nucleotides 1702-2104 of (S2) and/or nucleotides
1-97 of (S3) and/or nucleotides 367-1283 of (S3), or (iv) a combination
of any one of the nucleotide sequences of (S1)-(S3) or their portions.
(III) comprises a stretch of 50 nucleotides having at least 70% sequence
identity with a consecutive stretch of at least 50 nucleotides of

(S1)-(S3), (S17)-(S19) or to (F) as described above. (S1) is part of the 5' upstream sequence of rice chemically induced cDNA-1 (RCI-1) gene, (S2) is part of rice RCI-1 gene including putative TATA box and putative start codon, (S3) is part of the rice RCI-1 gene including part of intron 1, exon 2, intron 2 and part of exon 3, (S17) is nucleotide sequence of 4.5 kb PstI/PstI fragment from plasmid pBSK+lipoxxygenase (LOX)4A, (S18) is a part of the 5' upstream sequence of the rice RCI-1 gene obtained by PCR, and (S19) is a part of the 5' upstream sequence of the rice RCI-1 gene obtained by PCR. (I), (II), and (III) are capable of driving the expression of an associated nucleotide sequence when induced by a chemical inducer such as BTH (benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester), INA (2,6-dichloroisonicotinic acid) or probenazole. Preferably, (I) drives expression of a nucleotide sequence when induced by jasmonic acid. (IV) comprises the isolated nucleic acid operably linked to a polypeptide coding sequence that comprises at its 5' end a nucleotide sequence encoding a fully defined lipoxxygenase protein having the amino acid sequence of 37 amino acids as given in the specification. The coding sequence preferably encodes a desirable phenotypic trait. Optionally, the coding sequence is in antisense orientation. (X) preferably encodes a protein having a sequence of (S7). Preferred Host Cell: The host cell is a plant cell. Preferred Transformed Plant: The plant is a maize, wheat, sorghum, rye, oats, turf grass, rice, barley, soybean, cotton, tobacco, sugar beet or oilseed rape.

ACTIVITY - Plant antifungal. Details of test given but no results are stated.

MECHANISM OF ACTION - Fungal mycotoxin inhibitor. No data provided.

USE - (I), (II), (III) are useful for expressing a nucleotide sequence of interest. (IX) is useful for targeting an associated protein of interest to plastids. (X) which expresses polypeptide having lipoxxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. (XI) is useful for inhibiting fungal mycotoxins (claimed). (I) is useful for regulating transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical regulator to a plant or seed containing a chemically regulatable nucleotide sequence. Transgenic plants as described above are useful for breeding improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to their optimized genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

EXAMPLE - Cloning of the rice chemically induced cDNA (RCI)-1 promoter region was carried out as follows. A lambda-DASH II/BamHI library representing genomic DNA derived from *Oryza sativa* cv. Norin plants was constructed. Screening of the library was carried out. The library was plated on four 530 cm² bio-assay dishes. The plaques were transferred onto a nylon membrane. A 900 bp PstI-fragment representing the 5' end of the rice RCI-1 lipoxxygenase cDNA clone pRC-1 having a fully defined sequence of 3018 nucleotides (S5) as given in the specification, was labeled with 32P and hybridized overnight at 65degreesC to plaque lifts. Two additional rounds of screening resulted in a positive lambda-clone (lambda lipoxxygenase (LOX)4). The 4.5 kb DNA fragment was subcloned into a pBluescript/SK+vector and transformed into *Escherichia coli* strain DH5alpha cells and transformants were selected. This resulting clone was designated pBSK+LOX4A. Clone pBSK+LOX4A was deposited with the DSMZ with accession number DSM 13524. Clone pBSK+LOX4A contained the RCI-1 lipoxxygenase promoter on a 4.5 kb PstI/PstI fragment and was further analyzed by DNA sequencing. Clone pBSK+LOX4A comprise, in a 5' to 3' direction, the nucleotide sequences (S1), (S2) and (S3). (S1) comprises the 5' end of the 4.5 kb PstI/PstI fragment. This nucleotide sequence was 358 nucleotides in length and

contained at its 5' end in position 1 to 6 the PstI-site. The region between (S1) and (S2) of the 4.5 kb PstI/PstI fragment was between about 240 and 440 bp in length. The central region of the 4.5 bp PstI/PstI fragment was (S2) and was 2104 bp in length. It contained the putative TATA box (position 1261 to 1266 (S2)), the putative start codon (position 1359 to 1361 of (S2)), as well as the 5' untranslated region and nucleotide sequences upstream of the putative TATA box. Comparison of the genomic DNA (S2) and the cDNA (S5) showed that the sequences located at position 1312 to 1701 of (S2) comprised all or part of exon 1, and the sequences located at position 1702 to 2104 of (S2) were the 5' part of intron 1. The region between (S2) and (S3) of the 4.5 kb PstI/PstI fragment was between about 85 and 285 bp in length. The 3' end of the 4.5 kb PstI/PstI fragment was (S3). This sequence depicted a nucleotide sequence of 1516 bp in length. It contained, in a 5' to 3' end of intron 1 (position 1 to 97 of (S3)) followed by exon 2 (position 98 to 366 of (S3)), intron 2 (position 367 to 1283 of (S3)) and part of exon 3 (position 1284 to 1516 of (S3)). The PstI site was located at position 1511 to 1516. (88 pages)

ACCESSION NUMBER: 2002-10155 BIOTECHDS

TITLE: Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence;
recombinant vector plasmid pBSK-mediated lipoxxygenase gene transfer and expression in host cell and polymerase chain reaction for use as a fungicide, herbicide and pesticide

AUTHOR: DUDLER R; SCHAFFRATH; LAWTON K A
PATENT ASSIGNEE: SYNGENTA PARTICIPATIONS AG; UNIV ZUERICH
PATENT INFO: WO 2002006490 24 Jan 2002
APPLICATION INFO: WO 2000-EP8085 13 Jul 2000
PRIORITY INFO: GB 2000-22739 15 Sep 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-188550 [24]

L8 ANSWER 6 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to sugarbeet (Beta vulgaris) by introducing a DNA fragment having a nucleotide sequence which is homologous to the sequence of the genomic RNA-1 of BNYVV;
plasmid pVDH239 and plasmid pVDH240-mediated gene transfer and expression in transgenic plant

AN 2000-13300 BIOTECHDS

AB Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to a sugarbeet (Beta vulgaris) by introducing a DNA fragment of at least 15 bp in a sequence that is essentially homologous to the corresponding nucleotide sequence of the genomic RNA-1 of BNYVV. Also claimed are: a vector (plasmid pVDH239 and plasmid pVDH240) containing the DNA fragment; the use of the vector to transform plant cells using Agrobacterium tumefaciens; a plant cell containing the DNA fragment; the use of the plant cell for the regeneration of a sugarbeet that is resistant against BNYVV; a sugarbeet consisting at least partly of the plant cell; the progeny and seeds of the plant; and vegetatively reproducible structures such as calluses, buds and embryos derived from the sugar beet plant and seeds. The method is useful for conveying resistance to sugar beet plants against BNYVV and producing transgenic plants with complete immunity to BNYVV. Plant cells and other reproducible structures derived from these transgenic plants may be used for reproducing or regenerating subsequent generations of resistant sugar beet plants. (31pp)

ACCESSION NUMBER: 2000-13300 BIOTECHDS

TITLE: Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to sugarbeet (Beta vulgaris) by

introducing a DNA fragment having a
nucleotide sequence which is homologous to the sequence of
the genomic RNA-1 of BNYVV;
plasmid pVDH239 and plasmid pVDH240-mediated gene transfer
and expression in transgenic plant

AUTHOR: Richards K; Jonard G; Guillely H; van dun C M P
PATENT ASSIGNEE: SES-Europe
LOCATION: Tiennen, Belgium.
PATENT INFO: WO 2000044915 3 Aug 2000
APPLICATION INFO: WO 2000-EP609 26 Jan 2000
PRIORITY INFO: EP 1999-200236 27 Jan 1999
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2000-505981 [45]

L8 ANSWER 7 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN

TI DNA encoding scorpion peptide androctonin;
vector-mediated gene transfer and expression in host cell or
transgenic plant, used to confer disease-resistance

AN 1999-06262 BIOTECHDS

AB A new DNA fragment encodes androctonin (AD). Also
new are: a DNA fragment encoding a peptide-AD or
AD-peptide fusion protein; a fusion protein encoded
by the DNA; a chimeric gene consisting of the new DNA linked to
expression regulatory sequences; a cloning or expression vector
containing the chimeric DNA; a host cell (preferably a plant cell)
transformed with the vector; plants containing the transformed cells; and
seeds of the transgenic plant. The DNA can be used to produce transgenic
plants with disease-resistance against bacterial or fungal infections,
especially infection caused by *Cercospora beticola*, *Cladosporium*
herbarum, *Fusarium cuulmorum*, *Fusarium graminearum* or *Phytophthora*
cinnamomi. The host cell may be a bacterium such as *Escherichia coli*, a
yeast such as *Saccharomyces* sp., *Kluyveromyces* sp. or *Pichia* sp., a
fungus such as *Aspergillus* sp., a baculo virus or a plant cell. The
transgenic plant may be maize (*Zea mays*), wheat (*Triticum aestivum*), rape
(*Brassica napus*), soybean (*Glycine max*), rice (*Oryza sativa*), sugarcane
(*Saccharum officinale*), sugarbeet (*Beta vulgaris*),
tobacco (*Nicotiana tabacum*) or cotton (*Gossypium hirsutum*). (37pp)

ACCESSION NUMBER: 1999-06262 BIOTECHDS

TITLE: DNA encoding scorpion peptide androctonin;
vector-mediated gene transfer and expression in host cell
or transgenic plant, used to confer disease-resistance

AUTHOR: Freyssinet G; Deroose R; Hoffmann J

PATENT ASSIGNEE: Rhone-Poulenc-Agrochem.

LOCATION: Lyons, France.

PATENT INFO: WO 9909189 25 Feb 1999

APPLICATION INFO: WO 1998-FR1814 18 Aug 1998

PRIORITY INFO: FR 1997-10632 20 Aug 1997

DOCUMENT TYPE: Patent

LANGUAGE: French

OTHER SOURCE: WPI: 1999-181046 [15]

L8 ANSWER 8 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN

TI DNA fragment encoding alpha-amylase in dicotyledonous
plant;

fusion protein gene cloning and controlled expression in
'*Escherichia coli*, *Bacillus subtilis*, *Aspergillus* sp., *Agrobacterium*
sp. or potato; DNA probe construction; DNA sequence

AN 1991-02153 BIOTECHDS

AB The following are claimed: an AmyZ4 or AmyZ6 gene (A) from a
dicotyledonous plant, encoding an alpha-amylase (EC-3.2.1.1), and with
regulatory regions, a promoter, a coding region, introns and
transcription terminators, possibly labeled; DNA encoding a fusion

protein, with (A) and at least 1 other polypeptide gene; a purified polypeptide, encoded by (A) and free of other naturally occurring enzymes; DNA encoding an antisense RNA complementary to (A) mRNA and inhibiting its translation; antisense DNA for (A) under the control of a promoter for production of antisense RNA; single-stranded DNA or RNA complementary to either strand of (A); a vector carrying any of these fragments; a host, e.g. *Bacillus subtilis*, *Saccharomyces cerevisiae*, *Aspergillus* sp., *Agrobacterium* sp. or (preferably) *Escherichia coli* K12 (DSM 5275, DSM 5276, DSM 5882, DSM 5883, or DSM 5884) or a transgenic plant, preferably potato (*Solanum tuberosum*), containing (A); and methods for production of these. (A) is used for controlled expression of alpha-amylase activity, and is useful as a DNA probe for quantification of (A) mRNA for use e.g. in the food and alcohol industries. (155pp)

ACCESSION NUMBER: 1991-02153 BIOTECHDS

TITLE: DNA fragment encoding alpha-amylase in dicotyledonous plant; fusion protein gene cloning and controlled expression in *Escherichia coli*, *Bacillus subtilis*, *Aspergillus* sp., *Agrobacterium* sp. or potato; DNA probe construction; DNA sequence

PATENT ASSIGNEE: Danisco

PATENT INFO: WO 9012876 1 Nov 1990

APPLICATION INFO: WO 1990-DK108 24 Apr 1990

PRIORITY INFO: DK 1989-1980 24 Apr 1989

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 1990-348479 [46]

L8 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN

TI Elimination of transcriptional interference between tandem genes in plant cells

AB This invention relates to the field of biotechnol. or genetic engineering. Specifically, this invention relates to the field of gene expression. More specifically, this invention relates to methods to reduce or eliminate transcriptional interference between two or more tandemly arranged genes within a host cell.

ACCESSION NUMBER: 2002:814750 HCAPLUS

DOCUMENT NUMBER: 137:334040

TITLE: Elimination of transcriptional interference between tandem genes in plant cells

INVENTOR(S): Padidam, Malla

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 33 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002155540	A1	20021024	US 2002-74744	20020213
PRIORITY APPLN. INFO.:			US 2001-268584P	P 20010214

L8 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN

TI PCR-based cloning and segregation analysis of functional gene homologues in *Beta vulgaris*

AB To analyze genetic factors that potentially affect sugar quality and yield in *Beta vulgaris*, we designed primers based on 18 homologous ESTs and conserved regions of 32 heterologous ESTs encoding gene products that act in the Calvin cycle, the oxidative pentose phosphate cycle, photorespiration, synthesis, transport and degradation of

sucrose, glycolysis, the citric acid cycle, nitrogen metabolism and osmoprotection. Data on the amplification of 54 gene homologues from *B. vulgaris* are presented. Among these are 35 homologues for which DNA sequence information from *B. vulgaris* is now available for the first time. For genetic mapping a PCR-based strategy using CAPS (cleaved amplified polymorphic sequence), DFLP (DNA fragment length polymorphism), SSCP (single-strand conformation polymorphism) and HD (heteroduplex) anal. was adopted. RFLP anal. was also used in some cases. The different techniques used for the detection of polymorphisms are evaluated with respect to their sensitivity and versatility. In all, 42 functional genes have been assigned to the nine linkage groups of sugar beet.

ACCESSION NUMBER: 1999:796844 HCAPLUS
DOCUMENT NUMBER: 132:147436
TITLE: PCR-based cloning and segregation analysis of functional gene homologues in *Beta vulgaris*
AUTHOR(S): Schneider, K.; Borchardt, D. C.; Schafer-Pregl, R.; Nagl, N.; Glass, C.; Jeppsson, A.; Gebhardt, C.; Salamini, F.
CORPORATE SOURCE: Max-Planck-Institut fur Zuchtforschung, Koln, D-50829, Germany
SOURCE: Molecular and General Genetics (1999), 262(3), 515-524
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

Refine Search

Search Results -

Terms	Documents
L8 and L5	866

Database:

US Pre-Grant Publication Full-Text Database

US Patents Full-Text Database

US OCR Full-Text Database

EPO Abstracts Database

JPO Abstracts Database

Derwent World Patents Index

IBM Technical Disclosure Bulletins

Search:

L9

Refine Search

Recall Text

Clear

Interrupt

Search History

DATE: Tuesday, August 29, 2006

[Purge Queries](#)

[Printable Copy](#)

[Create Case](#)

Set Name Query

side by side

Hit Count Set Name

result set

DB=PGPB; PLUR=YES; OP=OR

L9 L8 and l5

866

L9

L8 allen.in.

6781

L8

DB=USPT; PLUR=YES; OP=OR

L7 L5 and (sugar transport protein)

0

L7

L6 L5 and (DNA encoding protein)

0

L6

DB=PGPB; PLUR=YES; OP=OR

L5 beta vulgaris

138458

L5

L4 L1 and (beta vulgaris)

1

L4

L3 L1 and (90%)

1

L3

L2 L1 and (isolated cell)

1

L2

L1 20020178468

1

L1

END OF SEARCH HISTORY

Refine Search

Search Results -

Terms	Documents
6383776.pn.	1

Database:

US Pre-Grant Publication Full-Text Database

US Patents Full-Text Database

US OCR Full-Text Database

EPO Abstracts Database

JPO Abstracts Database

Derwent World Patents Index

IBM Technical Disclosure Bulletins

Search:

L18

Refine Search

Recall Text



Clear

Interrupt

Search History

DATE: Tuesday, August 29, 2006

[Purge Queries](#)

[Printable Copy](#)

[Create Case](#)

Set Name Query

side by side

Hit Count

Set Name

result set

DB=USPT; PLUR=YES; OP=OR

L18 6383776.pn. 1 L18

L17 7041476.pn. 1 L17

DB=USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR

L16 L15 0 L16

DB=PGPB; PLUR=YES; OP=OR

L15 L14 and (DNA complement) 346 L15

L14 L13 and (transform cell) 366 L14

L13 L12 and (regulatory sequence) 366 L13

L12 L11 and (fragment) 371 L12

L11 L10 and (DNA encoding protein) 561 L11

L10 L9 and (sugar transport protein) 651 L10

L9 L8 and l5 866 L9

L8 allen.in. 6781 L8

DB=USPT; PLUR=YES; OP=OR

L7 L5 and (sugar transport protein) 0 L7

L6 L5 and (DNA encoding protein) 0 L6

DB=PGPB; PLUR=YES; OP=OR

L5 beta vulgaris 138458 L5

L4 L1 and (beta vulgaris) 1 L4

<u>L3</u>	L1 and (90%)	1	<u>L3</u>
<u>L2</u>	L1 and (isolated cell)	1	<u>L2</u>
<u>L1</u>	20020178468	1	<u>L1</u>

END OF SEARCH HISTORY